more than insoluble fiber, and malabsorption of fat can be attributed to deconjugation of bile acids.

Key Words: dietary fiber, fat digestibility, bile acids

W118 The gut and vaginal microbiota profile of pregnant sows and their contribution to neonatal piglet gut microbiota development. Alessi A. Kwawukume*, Hein M. Tun, Martin C. Nyachoti, and Ehsan Khafipour, *University of Manitoba, Winnipeg, Manitoba, Canada.*

The establishment of an initial gut microbiota is identified as a critical stage in neonatal development and is believed to influence health throughout life. Neonates are believed to receive their first bacterial colonizers while passing through the birth canal, from the environment as well as from milk during suckling; however, the relationship between maternal microbiota and development of neonatal gut microbiota is not clearly understood. To establish the contribution of maternal microbiota (gut and vaginal) to neonatal gut microbiota development, swab samples were taken from the posterior and anterior vagina 4 d before expected farrowing in pregnant sows housed on concrete slatted floors (CSF) (n = 12) and on straw (ASF) (n = 15). Fecal samples were obtained from sows at the same time as vaginal sampling, and from 5 piglets born to each sow (n = 135 piglets) on d 0, 1 and 3 after birth. DNA was extracted and subjected to V3-V4 bacterial 16S rRNA Illumina sequencing. Firmicutes (46.5%) and Bacteroidetes (24.8%) dominated the vaginal bacterial community of pregnant sows while Proteobacteria were in low numbers (14.5%). Among Firmicutes, Clostridia (34.6%) were found to predominate while Lactobacilli (3.8%) were few. No differences in β-diversity ($P = 0.447$) of bacterial communities were observed between the anterior and posterior vagina in sows from the 2 housing types. Firmicutes and Bacteroidetes dominated sows fecal microbiota (48.7% and 37.13% respectively) with relatively low numbers of Proteobacteria (0.9%). Fecal samples of piglets differed in percent composition during the first 3 d after birth. Proteobacteria were found to be predominant on d 0 (63.8%), Firmicutes on d 1 (55.2%), and Firmicutes and Bacteroidetes on d 3 (60.1% and 15.15% respectively). Although piglet fecal microbiota was significantly different from both sow vaginal, and fecal microbiota ($P = 0.001$), the principal coordinate analysis showed a moving trend of piglet microbiota toward the sow vaginal microbiota as piglets grew from d 1 to d 3. Results indicate that maternal microbiota may contribute to piglet gut microbiota development.

Key Words: piglet, sow, vaginal and fecal microbiota

W119 Enteral bile acids modulate intestinal immune response and gut microbiota in early-weaned piglets challenged with LPS. Alessandro Mereu*[1], Nuria de Diego-Cabero[2], Jose Javier Pastor Porras[1], David Menoyo[2], and Ignacio Ipharraguerre[3,1], *[1]Lucta SA, Montornés del Valles, Barcelona, Spain, [2]Departamento de Producción Animal, Universidad Politécnica de Madrid, ETS Ingenieros Agrónomos, Madrid, Spain, [3]Institute of Human Nutrition and Food Science, University of Kiel, Kiel, Germany.*

Bile acids (BA) have recently emerged as regulators of intestinal immune homeostasis and mucosal integrity. We examined the effects of administering enterally deoxycholic acid (DCA) to early-weaned pigs challenged with lipopolysaccharide (LPS) on gut BA profile, immune response and microbiota. Twenty-four piglets were weaned at 21 d, acclimatized for 14 d, and subsequently grouped (n = 8) to be intragastrically infused with either deionized water (C+, C−) or 15 mg of DCA·kg^{-1} initial BW (DCA) daily during 14 d. On d 28, C+ and DCA piglets were injected i.p. with 150 μg LPS·kg^{-1} BW. Three h later, all animals were bled and killed for organ measurement and sampling. Blood samples were analyzed for endotoxin (EDT), interleukin (IL)-6, and tumor necrosis factor α (TNF-α). Expression of occludin, IL-6 and IL-10 genes and the concentration of individual BA were measured in the ileal mucosa. Colonic microbiota was characterized by sequencing bacterial 16S ribosomal-RNA. Individual BW and feed intake were recorded weekly. Data were analyzed with a mixed-effects model in which pig was treated as random effect and treatment as fixed effect. Compared with C-, LPS decreased total BA concentration ($P < 0.01$) and increased plasma TNF-α ($P < 0.01$) and EDT ($P < 0.02$) as well as hepatic ($P < 0.01$) and intestinal ($P < 0.03$) weight. Interestingly, DCA infusion increased the proportion of BA with the greatest ability to induce BA-signaling pathways ($P < 0.05$), prevented alterations ($P > 0.10$) in plasma EDT and intestinal weight, decreased expression of IL genes ($P < 0.04$) in the ileum, and enhanced ($P < 0.05$) feed intake. In addition, treating pigs with DCA increased ($P < 0.05$) *Peptostreptococcaceae* and *Clostridiaceae* whereas decreased ($P < 0.05$) *Lactobacillaceae* in the colon. In conclusion, DCA acted locally to prevent LPS-induced inflammation and barrier disruption of the intestinal mucosa. These effects were associated with changes in the intestinal BA signature.

Key Words: deoxycholic acid, bile acid signaling, gut permeability

W120 Impact of xylanases on gut microbiome of growing pigs fed with corn-based and wheat-based diets. H. M. Tun*[1], R. Li[1], E. Kiarie[1,2], M. Nyachoti[1], and E. Khafipour[1], *[1]University of Manitoba, Winnipeg, MB, Canada, [2]DuPont Industrial Biosciences-Danisco Animal Nutrition, Marlborough, Wiltshire, UK.*

This study was carried out to assess the effects of exogenous xylanases on production performance and gastrointestinal microbiota of growing gilts fed corn-based or wheat-based diets. A total of 96 individually penned gilts (22.7 ± 0.65 kg initial BW) were used in a CRD experiment with 2 × 6 factorial arrangement and fed experimental diets for 42 d. Gilts (n = 8 per treatment) received one of the 2 basal diets: (a) corn with 40% corn distillers dried grains, or (b) wheat with 25% wheat co-products, each without or with one of the 5 xylanases (XA, XB, XC, XD and XE). Xylanases were supplemented at 75 mg/kg of feed and all diets contained phytase. All xylanases were produced by different fungal organisms, except for xylanase-C, which originated from bacteria. On d 42, all pigs were euthanized to obtain ileal and cecum digesta for microbiome analysis using pyrosequencing of V1-V3 regions of 16S rRNA and downstream bioinformatic analyses using QIIME. Spearman's correlation was used to correlate microbiome composition data with performance characteristics, apparent total-tract digestibility (ATTD), and colon digesta volatile fatty acids (VFA) concentration. The XA yielded the best growth performance in both corn and wheat based diets ($P < 0.05$) when compared with other xylanases. Based on PERMANOVA analysis on UniFrac distances, XA significantly affected the β-diversity of ileum microbiota compared with other xylanases and controls ($P < 0.05$). Furthermore, xylanases influenced ATTD and colonic digester volatile fatty acids diet dependently ($P < 0.05$). The XA increased *Lactobacillus* species in the cecum in both diets, whereas other xylanases drastically decreased *Lactobacillus* species when compared with control ($P < 0.05$). In the wheat-based diet with xylanases, cecal bacterial community composition changes significantly correlated with ATTD of DM ($r = −0.5$), gross energy digestibility ($r = −0.49$) and colon VFA concentrations ($r = −0.67$) ($P < 0.02$). However, in the corn-based diet with xylanases, ileal bacterial community changes correlated with ATTD of DM ($r = −0.4$) and gross energy digestibility ($r = −0.43$), whereas cecal bacterial community changes correlated with